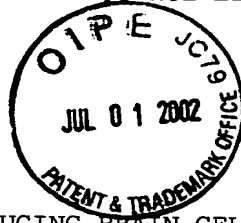


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TECH CENTER 1600/2900

## SEQUENCE LISTING



<110> Chiorini, John  
Kotin, Robert M.  
Safer, Brian  
Davidson, Elizabeth  
Zabner, Joseph

<120> AAV5 VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS

<130> 14014.0323U2

<140> 09/533,427

<141> 2000-03-22

<160> 26

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 4652

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 1

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tgttttatcc	aataggaaga	aagcgcgcgt	atgagttctc	gcgagacttc	cggggtataa	300
aagaccgagt	gaacgagccc	gccgccattc	tttgctctgg	actgctagag	gaccctcgct	360
gccatggcta	ccttctatga	agtcattgtt	cgcgctccat	ttgacgtgga	ggaacatctg	420
cctggaattt	ctgacagctt	tgtggactgg	gtaactggtc	aaatttggga	gctgcctcca	480
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cagtttgaaa	agggatctga	atattttcat	ctgcacacgc	ttgtggagac	ctccggcatc	660
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cagctcaaaag	agctgccaga	cgacggccct	ctggccgtcg	cccccccaaa	cgagccagcg	4620
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&lt;210&gt; 2

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 2

Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys

1

5

10

15

Gln	Trp	Ile	Gln	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr
		20						25					30		
Gly	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser
	50					55					60				
Val	Pro	Glu	Asp	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met
	65				70					75					80
Asn	Gly	Tyr	Asp	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys
			85					90						95	
Gln	Arg	Ser	Phe	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala
			100					105						110	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn
	145				150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
	195					200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Lys	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
	225				230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
			245					250						255	
Thr	His	Glu	Phe	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala
			260					265					270		
Glu	Lys	Ser	Leu	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr
	275					280						285			
Lys	Ser	Leu	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro
	290					295					300				
Arg	Ser	Ser	Asp	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
	305				310					315					320
Trp	Asn	Ser	Arg	Tyr	Asp	Cys	Lys	Cys	Asp	Tyr	His	Ala	Gln	Phe	Asp
			325						330					335	
Asn	Ile	Ser	Asn	Lys	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys
			340					345					350		
Asn	Gly	Cys	Ile	Cys	His	Asn	Val	Thr	His	Cys	Gln	Ile	Cys	His	Gly
	355					360						365			
Ile	Pro	Pro	Trp	Glu	Lys	Glu	Asn	Leu	Ser	Asp	Phe	Gly	Asp	Phe	Asp
	370					375					380				
Asp	Ala	Asn	Lys	Glu	Gln										
	385				390										

&lt;210&gt; 3

&lt;211&gt; 610

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 3

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1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25					30		
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val
		35					40				45				
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
	50					55					60				
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
65				70						75				80	
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
			85						90					95	
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
			100					105					110		
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn
	115							120					125		
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val
	130					135					140				
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro
145					150					155				160	
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala
			165						170					175	
Leu	Asn	Leu	Glu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu
		180						185					190		
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala
	195					200						205			
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val
	210					215					220				
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
225					230					235				240	
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
			245						250					255	
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
		260						265					270		
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
	275						280					285			
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
	290					295					300				
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
305				310						315				320	
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
			325						330					335	
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
		340						345					350		
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
	355						360					365			
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
	370					375					380				
Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
385					390					395				400	
Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser
			405						410					415	
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
		420						425					430		
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys
	435						440					445			
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp
	450					455					460				
Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe
465					470					475				480	

●

5

Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp		
				245					250					255			
Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr		
			260					265					270				
Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	Gln		
		275					280					285					
Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val		
	290				295					300							
Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	Thr		
305				310						315					320		
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp		
				325					330					335			
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys		
			340					345					350				
Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr		
		355				360						365					
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser		
		370			375						380						
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn		
385				390					395						400		
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser		
				405				410						415			
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp		
			420					425					430				
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln		
		435				440						445					
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp		
	450			455							460						
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly		
465				470					475						480		
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu		
				485				490						495			
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr		
			500					505					510				
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile		
		515					520					525					
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu		
	530					535					540						
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg		
545				550						555					560		
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser		
				565				570						575			
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro		
			580					585						590			
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp		
		595				600						605					
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met		
	610					615					620						
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn		
625				630						635					640		
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser		
				645				650						655			
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu		
			660					665					670				
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln		
		675					680					685					
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp		
	690					695					700						
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu		
705					710					715					720		
Thr	Arg	Pro	Leu														

<210> 5  
 <211> 588  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 5

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Lys	Ala	Arg	Thr	Glu	Glu	Asp	Ser	Lys	Pro	Ser	Thr	Ser	Ser	Asp	Ala
			20					25					30		
Glu	Ala	Gly	Pro	Ser	Gly	Ser	Gln	Gln	Leu	Gln	Ile	Pro	Ala	Gln	Pro
		35					40					45			
Ala	Ser	Ser	Leu	Gly	Ala	Asp	Thr	Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro
	50					55					60				
Leu	Gly	Asp	Asn	Asn	Gln	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly
65					70					75					80
Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys
				85					90					95	
Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg
			100					105					110		
Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe
		115					120					125			
Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser
	130					135					140				
His	Trp	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly
145					150					155					160
Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys
				165					170					175	
Glu	Val	Thr	Val	Gln	Asp	Ser	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr
			180					185					190		
Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val
		195					200					205			
Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val
	210					215					220				
Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr
225					230					235					240
Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro
				245					250					255	
Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe
		260						265					270		
Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe
		275					280					285			
Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser
	290					295					300				
Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg
305					310					315					320
Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr
				325					330					335	
Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala
		340						345					350		
Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val
		355					360					365			
Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr
	370					375					380				

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Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn Pro
385                      390                      395                      400
Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser Glu
                      405                      410                      415
Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly Gln
                      420                      425                      430
Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly Thr
                      435                      440                      445
Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg Asp
                      450                      455                      460
Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala
465                      470                      475                      480
His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro
                      485                      490                      495
Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr
                      500                      505                      510
Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr
                      515                      520                      525
Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser
                      530                      535                      540
Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro
545                      550                      555                      560
Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr
                      565                      570                      575
Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                      580                      585

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&lt;210&gt; 6

&lt;211&gt; 532

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 6

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Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
                      20                      25                      30
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
                      35                      40                      45
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
50                      55                      60
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65                      70                      75                      80
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
                      85                      90                      95
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
                      100                      105                      110
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
                      115                      120                      125
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
130                      135                      140
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
145                      150                      155                      160
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
                      165                      170                      175
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
                      180                      185                      190

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Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	
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Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser	
	210					215					220					
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	
225					230					235					240	
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	
				245					250					255		
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	
			260					265					270			
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	
		275					280					285				
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	
	290					295					300					
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	
305					310					315					320	
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	
				325					330					335		
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu	
			340					345					350			
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg	
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Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser	
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Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro	
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Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	
				405					410					415		
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met	
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Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	
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Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	
	450					455					460					
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu	
465					470					475					480	
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	
				485					490					495		
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	
			500					505					510			
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	
		515					520					525				
Thr	Arg	Pro	Leu													
			530													

&lt;210&gt; 7

&lt;211&gt; 2307

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 7

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cgggcccacc	gaaacaaaa	cccaatcagc	agcatcaaga	tcaagcccgt	ggtcttgtgc	240
tgcctggtta	taactatctc	ggacccggaa	acggtctcga	tcgaggagag	cctgtcaaca	300
gggcagacga	ggtcgcgcga	gagcacgaca	tctcgtacaa	cgagcagctt	gaggcgggag	360

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aaccttttgg	cctggttgaa	gaggggtgcta	agacggcccc	taccggaaaag	cggatagacg	540
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&lt;210&gt; 8

&lt;211&gt; 2264

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 8

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&lt;210&gt; 9

&lt;211&gt; 2264

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 9

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gctgccctac	gtcgtcggca	acgggaccga	gggatgcctg	ccggccttcc	ctccgcaggt	1140
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cacgtacctc	gagggcaaca	tgctcatcac	cagcgagagc	gagacgcagc	cggatgaaccg	1740

cgtggcgtag	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
cgcgaccggc	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagagggg	1860
cgtgtacctc	caaggaccca	tctggggcaa	gatcccagag	acggggggcg	actttcaccc	1920
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&lt;210&gt; 10

&lt;211&gt; 1292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 10

agcgcaaacg	gctcgtcgcg	cagtttcttg	cagaatcctc	gcagcgctcg	caggaggcgg	60
cttcgcagcg	tgagttctcg	gctgaccggg	tcatcaaaag	caagacttcc	cagaaataca	120
tggcgctcgt	caactggctc	gtggagcagc	gcataccttc	cgagaagcag	tggatccagg	180
aaaatcagga	gagctacctc	tccttcaact	ccaccggcaa	ctctcggagc	cagatcaagg	240
ccgcgctcga	caacgcgacc	aaaattatga	gtctgacaaa	aagcgcggtg	gactacctcg	300
tggggagctc	cgttcccag	gacatttcaa	aaaacagaa	ctggcaaatt	tttgagatga	360
atggctacga	cccggcctac	gcgggatcca	tcctctacgg	ctggtgtcag	cgctccttca	420
acaagaggaa	caccgtctgg	ctctacggac	ccgccacgac	cggcaagacc	aacatcgcg	480
aggccatcgc	ccacactgtg	cccttttacg	gctgcgtgaa	ctggaccaat	gaaaactttc	540
cctttaatga	ctgtgtggac	aaaatgctca	tttgggtggg	ggaggggaa	atgaccaaca	600
aggtggttga	atccgccaa	gccatcctgg	ggggctcaaa	ggtgcgggtc	gatcagaaat	660
gtaaatcctc	tgttcaaatt	gattctaccc	ctgtcattgt	aacttccaat	acaaacatgt	720
gtgtggtggt	ggatgggaat	tccacgacct	ttgaacacca	gcagccgctg	gaggaccgca	780
tgttcaaatt	tgaactgact	aagcggtctc	cgccagattt	tggcaagatt	actaagcagg	840
aagtcaagga	cttttttgc	tgggcaaagg	tcaatcagg	gccggtgact	cacgagttta	900
aagttcccag	ggaattggcg	ggaactaaag	gggcggagaa	atctctaaaa	cgcccactgg	960
gtgacgtcac	caatactagc	tataaaagtc	tggagaagcg	ggccaggctc	tcatttgttc	1020
ccgagacg	tcgcagttca	gacgtgactg	ttgatcccgc	tcctctgcca	ccgtcgaatt	1080
ggaattcaag	gtatgattgc	aaatgtgact	atcatgctca	atttgacaac	atttctaaca	1140
aatgtgatga	atgtgaatat	ttgaatcggg	gcaaaaatgg	atgtatctgt	cacaatgtaa	1200
ctcactgtca	aatttgtcat	gggattcccc	cctgggaaaa	ggaaaacttg	tcagattttg	1260
gggattttga	cgatgccaat	aaagaacagt	aa			1292

&lt;210&gt; 11

&lt;211&gt; 1870

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 11

attcttttgc	ctggactgct	agaggaccct	cgtgcccattg	gctaccttct	atgaagtc	60
tgttcgcgct	ccatttgacg	tggaggaaca	tctgcctgga	atttctgaca	gcttctgga	120
ctgggttaact	ggtcaaat	gggagctgcc	tccagagtca	gattttaa	tgactctggt	180
tgaacagcct	cagttgacgg	tggtgatag	aattcgccgc	gtgttcctgt	acgagtggaa	240
caaattttcc	aagcaggagt	ccaaattctt	tgtgcagttt	gaaaagggat	ctgaatattt	300
tcatctgcac	acgcttgtgg	agacctccgg	catctcttcc	atggtcctcg	gccgctacgt	360
gagtcagatt	cgcgcccagc	tgggtgaaag	ggtcttccag	ggaattgaac	cccagatcaa	420

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cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg 480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtgagg cgtggacaaa 540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tctgcgcgca 600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tgcgagcgtg agttctcggc 660
tgacccgggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt 720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc 780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa 840
aattatgagt ctgacaaaaa gcgcgggtgga ctacctcgtg gggagctccg ttcccaggga 900
catttcaaaa aacagaatct ggcaaatatt tgagatgaat ggctacgacc cggcctacgc 960
gggatccatc ctctacggct ggtgtcagcg ctcttcaac aagaggaaca ccgtctggct 1020
ctacggaccc gccacgaccg gcaagaccaa catcgaggag gccatcgccc acactgtgcc 1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa 1140
aatgctcatt tgggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc 1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga 1260
ttctacccct gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc 1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaattg aactgactaa 1380
gcggctcccc ccagattttg gcaagattac taagcaggaa gtcaaggact ttttgcttg 1440
ggcaaagggt aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg 1500
aactaaaggg gcgggaaagt ctctaaaacg cccactgggt gacgtcacca atactagcta 1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga 1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaagg atgattgcaa 1680
atgtgactat catgctcaat ttgacaacat ttctaacaaa tgtgatgaat gtgaatattt 1740
gaatcggggc aaaaatggat gtatctgtca caatgtaact cactgtcaaa tttgtcatgg 1800
gattccccc tgggaaaagg aaaactgtgc agattttggg gattttgacg atgccataaa 1860
agaacagtaa 1870

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&lt;210&gt; 12

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 12

```

Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1           5           10           15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
          20           25           30

Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
          35           40           45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
          50           55           60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
          65           70           75           80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
          85           90           95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          130          135          140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
          145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
          180          185          190

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Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
    195                                200                205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                                215                220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
    225                                230                235                240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
    245                                250                255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
    260                                265                270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
    275                                280                285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                                295                300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
    305                                310                315                320
Trp Asn Ser Arg Leu Val Gly Arg Ser Trp
    325                                330

```

<210> 13  
 <211> 1115  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

```

<400> 13
aggagcgcaa acggctcgtc ggcagtttc tggcagaatc ctgcgagcgc tcgcaggagg      60
cggcttcgca gcgtgagttc tcggttgacc cggatcatcaa aagcaagact tcccagaaat      120
acatggcgct cgtcaactgg ctctgtggagc acggcatcac ttccgagaag cagtggatcc      180
aggaaaatca ggagagctac ctctccttca actccaccgg caactctcgg agccagatca      240
aggccgcgct cgacaacgcg accaaaatta tgagtctgac aaaaagcgcg gtggactacc      300
tcgtggggag ctccgttccc gaggacattt caaaaaacag aatctggcaa atttttgaga      360
tgaatggcta cgaccgggcc tacgcgggat ccctcctcta cggctggtgt cagcgctcct      420
tcaacaagag gaacaccgtc tggctctacg gaccgcccac gaccggcaag accaacatcg      480
cggaggccat cgcccacact gtgccctttt acggctgcgt gaactggacc aatgaaaact      540
ttccctttta tgactgtgtg gacaaaatgc tcatttggtg ggaggaggga aagatgacca      600
acaaggtggt tgaatccgcc aaggccatcc tggggggctc aaaggtgcgg gtcgatcaga      660
aatgtaaata ctctgttcaa attgattcta cccctgtcat tgtaacttcc aatacaaaaca      720
tgtgtgtggt ggtggatggg aattccacga cttttgaaca ccagcagccg ctggaggacc      780
gcatgttcaa atttgaactg actaagcggc tcccgccaga ttttggcaag attactaagc      840
aggaagtcaa ggactttttt gcttgggcaa aggtcaatca ggtgccggtg actcacgagt      900
ttaaagttcc cagggaattg gcgggaacta aaggggcgga gaaatctcta aaacgcccac      960
tgggtgacgt caccaatact agctataaaa gtctggagaa gcggggccagg ctctcatttg     1020
ttcccgagac gcctcgagt tcagacgtga ctgttgatcc cgctcctctg cgaccgctca     1080
attggaattc aagattggtt ggaagaagtt ggtga                                1115

```

<210> 14  
 <211> 550  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

```

<400> 14
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
    1              5              10              15

```

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly  
 20 25 30  
 Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val  
 35 40 45  
 Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu  
 50 55 60  
 Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln  
 65 70 75 80  
 Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr  
 85 90 95  
 Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg  
 100 105 110  
 Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn  
 115 120 125  
 Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val  
 130 135 140  
 Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro  
 145 150 155 160  
 Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala  
 165 170 175  
 Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu  
 180 185 190  
 Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala  
 195 200 205  
 Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val  
 210 215 220  
 Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln  
 225 230 235 240  
 Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg  
 245 250 255  
  
 Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu  
 260 265 270  
 Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp  
 275 280 285  
 Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp  
 290 295 300  
 Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe  
 305 310 315 320  
 Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys  
 325 330 335  
 Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys  
 340 345 350  
 Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys  
 355 360 365  
 Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu  
 370 375 380  
 Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys  
 385 390 395 400  
 Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser  
 405 410 415  
 Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu  
 420 425 430  
 His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys  
 435 440 445  
 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp  
 450 455 460  
 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe  
 465 470 475 480  
 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu  
 485 490 495

Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr	Lys	Ser	Leu	Glu
			500					505					510		
Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro	Arg	Ser	Ser	Asp
		515					520					525			
Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn	Trp	Asn	Ser	Arg
	530					535					540				
Leu	Val	Gly	Arg	Ser	Trp										
545					550										

<210> 15  
 <211> 1690  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 15  
 attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcac 60  
 tgttcgcgctc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga 120  
 ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt 180  
 tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa 240  
 caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatatatt 300  
 tcatctgcac acgcttgctg agacctccgg catctcttcc atggtcctcg gccgctacgt 360  
 gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa 420  
 cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg 480  
 gtatatcccg gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa 540  
 cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaaccgc tcgtcgcgca 600  
 gtttctggca gaatcctcgc agcgtctgca ggaggcggct tcgcagcgtg agttctcggc 660  
 tgaccgggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt 720  
 ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc 780  
 cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgcaca acgcgaccaa 840  
 aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg tttcccgagga 900  
 catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc 960  
 gggatccatc ctctacggct ggtgtcagcg ctcttccaac aagaggaaca ccgtctggct 1020  
 ctacggaccc gccacgaccg gcaagaccaa catcgcgag gccatcgccc acactgtgcc 1080  
 cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa 1140  
 aatgctcatt tgggtgggag agggaaagat gaccaacaag gtgggtgaat ccgccaaggc 1200  
 catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga 1260  
 ttctaccctt gtcattgtaa ctccaatac aaacatgtgt gtgggtgggtg atgggaattc 1320  
 cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa 1380  
 gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg 1440  
 ggcaaagggtc aatcagggtc cgggtgactca cgagtttaaa gttcccaggg aattggcggg 1500  
 aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta 1560  
 taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga 1620  
 cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaagat tggttggaag 1680  
 aagttggtga 1690

<210> 16  
 <211> 145  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 16  
 ccatcaccaa ggtaaagaag ggccggagcca ataaggtggt ggattctggg tatattcccg 60  
 cctacctgct gccgaaggct caaccggagc ttcagtgggc gtggacaaac ctggacgagt 120



ataaattggc cgccctgaat ctgga

145

&lt;210&gt; 17

&lt;211&gt; 174

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 17

taagcaggaa gtcaaggact tttttgcttg ggcaaagggtc aatcaggtgc cggtgactca	60
cgagttttaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg	120
cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag	174

&lt;210&gt; 18

&lt;211&gt; 187

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 18

cactctcaag caagggggtt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc	60
acgcgatagt taatgattaa cagtcattgt atgtgtttta tccaatagga agaaagcgcg	120
cgtatgagtt ctgcgcagac ttccggggta taaaagaccg agtgaacgag cccgccgcca	180
ttctttg	187

&lt;210&gt; 19

&lt;211&gt; 168

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 19

aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc	60
tcgtttgggg gggcgcagc tcaaagagct gccagacgac ggccctctgg ccgtcgcccc	120
cccaaacgag ccagcgagcg agcgaacgag acagggggga gaggcca	168

&lt;210&gt; 20

&lt;211&gt; 168

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 20

aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc	60
tcgtttgggg gggcgcagc cagagggccg tcgtctgccg gctctttgag ctgccacccc	120
cccaaacgag ccagcgagcg agcgaacgag acagggggga gaggcca	168

&lt;210&gt; 21

&lt;211&gt; 8



cggtgatcag	atcaaaaaact	tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	1020
aggggattac	ctcggagaag	cagtggatcc	aggaggacca	ggcctcatac	atctccttca	1080
atgcggcctc	caactcgcgg	tcccaaatac	aggctgcctt	ggacaatgcg	ggaaagatta	1140
tgagcctgac	taaaaccgcc	cccgactacc	tgggtggcca	gcagcccgtg	gaggacattt	1200
ccagcaatcg	gatttataaa	atthttggaac	taaacgggta	cgatcccca	tatgcggctt	1260
ccgtctttct	gggatgggcc	acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	1320
ggcctgcaac	taccgggaag	accaacatcg	cggaggccat	agcccacact	gtgcccttct	1380
acgggtgctg	aaactggacc	aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	1440
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tcggaggaag	caaggtgcgc	gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	1560
ctcccgtgat	cgtcacctcc	aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	1620
ccttcgaaca	ccagcagccg	ttgcaagacc	ggatgttcaa	atthgaactc	accgcctctc	1680
tggatcatga	ctttgggaag	gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	1740
aggatcacgt	ggttgagggtg	gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	1800
gacccgcccc	cagtgcgcga	gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	1860
agccatcgac	gtcagacgcg	gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	1920
gthctcgtca	cgtgggcatg	aatctgatgc	tgtttccctg	cagacaatgc	gagagaaatga	1980
atcagaattc	aaatatctgc	ttcactcacg	gcagaaaaga	ctgthtagag	tgctttcccg	2040
tgatcagaatc	tcaaccctgt	tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	2100
atcatatcat	gggaaagggtg	ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	2160
tggatgactg	catctttgaa	caataaatga	tttaaatcag	gtatggctgc	cgatggtht	2220
cttcagatt	ggctcgagga	cactctctct	gaaggaataa	gacagtgggtg	gaagctcaaa	2280
cctggccac	caccaccaa	gcccgcagag	cggcataagg	acgacagcag	gggtcttgtg	2340
cttcctgggt	acaagtacct	cggacccttc	aacggactcg	acaagggaga	gccggtcaac	2400
gaggcagacg	ccgcccct	cgagcacgta	caaagcctac	gaccggcagc	tcgacagcgg	2460
agacaacccg	tacctcaagt	acaaccacgc	cgacgcggag	tttcaggagc	gccttaagaa	2520
agatacgtct	tttgggggca	acctcggagc	agcagctctc	caggcgaaaa	agagggttct	2580
tgaacctctg	ggcctgggtg	aggaacctgt	taagacggct	ccgggaaaaa	agaggccggt	2640
agagcactct	cctgtggagc	cagactcctc	ctcgggaacc	ggaaaggcgg	gccagcagcc	2700
tgcaagaaaa	agattgaatt	ttggtcagac	tggagacgca	gactcagtag	ctgaccccca	2760
gcctctcgga	cagccaccag	cagccccctc	tggctctggga	actaatacga	tggctacagg	2820
cagtggcgca	ccaatggcag	acaataacga	gggcgcgcgac	ggagtgggta	attcctccgg	2880
aaattggcat	tgcgattcca	catggatggg	cgacagagtc	atcaccacca	gcacccgaac	2940
ctgggcccctg	cccacctaca	acaaccacct	ctacaaacaa	atthccagcc	aatcaggagc	3000
ctcgaacgac	aatcactact	ttggctacag	cacccttgg	gggtatthtg	acttcaacag	3060
attccactgc	cactthttcac	cagtgactgt	gcaaaagact	atcaacaaca	actggggatt	3120
ccgacccaag	agactcaact	tcaagctctt	taacattcaa	gtcaaaagag	tcacgcagaa	3180
tgacggtacg	acgacgattg	ccaataacct	taccagcacg	gttcagggtg	ttactgactc	3240
ggagtaccag	ctcccgtacg	tctcggctc	ggcgcatcaa	ggatgcctcc	cgccgttccc	3300
agcagacgtc	ttcatgggtg	cacagtatgg	atacctcacc	ctgaacaacg	ggagtccagg	3360
agtaggacgc	tcttcatttt	actgcctgga	gtactthtct	tctcagatgc	tgcgtaccgg	3420
aaacaacttt	accttcagct	acactthtga	ggagcttct	ttccacagca	gctacgtca	3480
cagccagagt	ctggaccgtc	tcatgaatcc	tctcatcgac	cagtacctgt	attacttgag	3540
cagaacaaac	actccaagt	gaaccaccac	gcagtcaagg	cttcagthtt	ctcaggccgg	3600
agcgagtac	attcgggacc	agtctaggaa	ctggcttct	ggaccctgtt	accgccagca	3660
gcgagtatca	aagacatctg	cggataacaa	caacagtgaa	tactcgtgga	ctggagctac	3720
caagtaccac	ctcaatggca	gagactctct	gggtgaatccg	gccatggcaa	gccacaagga	3780
cgatgaagaa	aagthttttc	ctcagagcgg	ggthtctatc	tttgggaagc	aaggctcaga	3840
gaaaacaaat	gtgaacattg	aaaaggctcat	gattacagac	gaagaggaaa	tcggaacaac	3900
caatcccgtg	gctacggagc	agtatggtht	tgtatctacc	aacctccaga	gaggcaacag	3960
acaagcagct	accgcagatg	tcaacacaca	aggcgtthct	ccaggcatgg	tctggcagga	4020
cagagatgtg	taccttcagg	ggcccatctg	ggcaaagatt	ccacacacgg	acggacattt	4080
tcacccctct	cccctcatgg	gtggattcgg	actthaaacac	cctcctccac	agattctcat	4140
caagaacacc	ccggtacctg	cgaatccttc	gaccaccttc	agtgcggcaa	agthtgcttc	4200
cttcatcaca	cagtactcca	cgggacacgg	tcagcgtgga	gatcgagtgg	gagctgcaga	4260
aggaacacag	caaacgctgg	aatcccga	ttcagtagac	ttcaactac	aacaagctctg	4320
ttaatcgtgg	gataactcgtg	gataactatg	gcgtgtattc	agagcctcgc	cccattggca	4380
ccagataacct	gactcgtaat	ctgtaattgc	ttgttaatca	ataaacctgt	taattcgttt	4440
cagttgaact	ttggtctctg	cgthtttctt	tcttatctag	thtccatggc	tacgtagata	4500
agtagcatgg	cgggttaatc	attaactaca	aggaacctct	agtgtggag	ttggccactc	4560
cctctctg	cgctcgtctg	ctcactgagg	ccgggcgacc	aaaggtcggc	cgacgcccg	4620

gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg gccaa

4675

<210> 25  
 <211> 735  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 25  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

&lt;210&gt; 26

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
 synthetic construct

&lt;400&gt; 26

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45

Glu 50	Gln	Ala	Pro	Leu	Thr	Val 55	Ala	Glu	Lys	Leu 60	Gln	Arg	Asp	Phe	Leu
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser	Gln	Ile
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn 140	Gly	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr
Met 225	Glu	Leu	Val	Gly 230	Trp	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr	Ile 250	Ser	Phe	Asn	Ala 255	Ala
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys
Ile	Met	Ser 275	Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Gln
Pro	Val 290	Glu	Asp	Ile	Ser	Ser 295	Asn	Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro
Phe	Tyr	Gly 355	Cys	Val	Asn	Trp	Thr 360	Asn	Glu	Asn	Phe	Pro 365	Phe	Asn	Asp
Cys	Val 370	Asp	Lys	Met	Val	Ile 375	Trp	Trp	Glu	Glu	Gly 380	Lys	Met	Thr	Ala
Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Thr 415	Pro	Val
Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser
Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln
Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480
Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Pro 495	Ala
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val
Ala	Gln	Pro 515	Ser	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu

530		535		540
Phe Pro Cys Arg Gln	Cys Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys		
545	550	555	560	
Phe Thr His Gly Gln	Lys Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu		
	565	570	575	
Ser Gln Pro Val Ser	Val Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr		
	580	585	590	
Ile His His Ile Met	Gly Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp		
	595	600	605	
Leu Val Asn Val Asp	Leu Asp Asp Cys Ile Phe	Glu Gln		
610	615	620		